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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/540,466DATE: 04/15/2000  
TIME: 09:48:39

Input Set: I540466.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: RIPAMONTI, UGO  
2 RAMOSHEBI, LENTSHA N.  
3 <120> TITLE OF INVENTION: METHODS FOR INDUCING ANGIOGENESIS USING MORPHOGENIC  
4 PROTEINS AND STIMULATORY FACTORS  
5 <130> FILE REFERENCE: STK-6  
6 <140> CURRENT APPLICATION NUMBER: US/09/540,466  
7 <141> CURRENT FILING DATE: 2000-03-31  
8 <160> NUMBER OF SEQ ID NOS: 10  
9 <170> SOFTWARE: PatentIn Ver. 2.1  
10 <210> SEQ ID NO 1  
11 <211> LENGTH: 1822  
12 <212> TYPE: DNA  
13 <213> ORGANISM: Homo sapiens  
14 <220> FEATURE:  
15 <221> NAME/KEY: CDS  
16 <222> LOCATION: (49)..(1341)  
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19 Met His Val  
20 1  
21 cgc tca ctg cga gct gca 105  
22 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala  
23 5 10 15  
24 ccc ctg ttc ctg ctg cgc tcc gcc ctg gcc gac ttc agc ctg gac aac 153  
25 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn  
26 20 25 30 35  
27 gag gtg cac tcg agc ttc atc cac cgg cgc ctc cgc agc cag gag cgg 201  
28 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg  
29 40 45 50  
30 cgg gag atg cag cgc gag atc ctc tcc att ttg ggc ttg ccc cac cgc 249  
31 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg  
32 55 60 65  
33 ccg cgc ccc cac ctc cag ggc aag cac aac tcg gca ccc atg ttc atg 297  
34 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met  
35 70 75 80  
36 ctg gac ctg tac aac gcc atg gcg gtg gag gag ggc ggc ggg ccc ggc 345  
37 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Pro Gly  
38 85 90 95  
39 ggc cag ggc ttc tcc tac ccc tac aag gcc gtc ttc agt acc cag ggc 393  
40 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly  
41 100 105 110 115  
42 ccc cct ctg gcc agc ctg caa gat agc cat ttc ctc acc gac gcc gac 441  
43 Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp  
44 120 125 130

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45	atg gtc atg agc ttc gtc aac ctc gtg gaa cat gac aag gaa ttc ttc	489
46	Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe	
47	135 140 145	
48	cac cca cgc tac cac cat cga gag ttc cgg ttt gat ctt tcc aag atc	537
49	His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile	
50	150 155 160	
51	cca gaa ggg gaa gct gtc acg gca gcc gaa ttc cgg atc tac aag gac	585
52	Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp	
53	165 170 175	
54	tac atc cgg gaa cgc ttc gac aat gag acg ttc cgg atc agc gtt tat	633
55	Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr	
56	180 185 190 195	
57	cag gtg ctc cag gag cac ttg ggc agg gaa tcg gat ctc ttc ctg ctc	681
58	Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu	
59	200 205 210	
60	gac agc cgt acc ctc tgg gcc tcg gag gag ggc tgg ctg gtg ttt gac	729
61	Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp	
62	215 220 225	
63	atc aca gcc acc agc aac cac tgg gtg gtc aat ccg cgg cac aac ctg	777
64	Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu	
65	230 235 240	
66	ggc ctg cag ctc tcg gtg gag acg ctg gat ggg cag agc atc aac ccc	825
67	Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro	
68	245 250 255	
69	aag ttg gcg ggc ctg att ggg cgg cac ggg ccc cag aac aag cag ccc	873
70	Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro	
71	260 265 270 275	
72	ttc atg gtg gct ttc aag gcc acg gag gtc cac ttc cgc agc atc	921
73	Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile	
74	280 285 290	
75	cgg tcc acg ggg agc aaa cag cgc agc cag aac cgc tcc aag acg ccc	969
76	Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro	
77	295 300 305	
78	aag aac cag gaa gcc ctg cgg atg gcc aac gtg gca gag aac agc agc	1017
79	Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser	
80	310 315 320	
81	agc gac cag agg cag gcc tgt aag aag cac gag ctg tat gtc agc ttc	1065
82	Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe	
83	325 330 335	
84	cga gac ctg ggc tgg cag gac tgg atc atc gcg cct gaa ggc tac gcc	1113
85	Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala	
86	340 345 350 355	
87	gcc tac tac tgt gag ggg gag tgt gcc ttc cct ctg aac tcc tac atg	1161
88	Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met	
89	360 365 370	
90	aac gcc acc aac cac gcc atc gtg cag acg ctg gtc cac ttc atc aac	1209
91	Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn	
92	375 380 385	
93	ccg gaa acg gtg ccc aag ccc tgc tgt gcg ccc acg cag ctc aat gcc	1257
94	Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala	

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Input Set: I540466.RAW

95	390	395	400	
96	atc tcc gtc ctc tac ttc gat gac agc tcc aac gtc atc ctg aag aaa			1305
97	Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys			
98	405	410	415	
99	tac aga aac atg gtg gtc cggtt ggc tgc cac tagtcctcc			1351
100	Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His			
101	420	425	430	
102	gagaatttcag accctttggg gccaagttt tctggatcct ccattgctcg cttggccag			1411
103	gaaccagcag accaactgcc ttttgtgaga cttcccccctc cctatccccca actttaaagg			1471
104	tgtgagagta ttaggaaaca tgagcagcat atggctttt atcagttttt cagtggcagc			1531
105	atccaatgaa caagatccta caagctgtgc aggcaaaacc tagcaggaaa aaaaaacaaac			1591
106	gcataaagaa aaatggccgg gccaggtcat tggctgggaa gtctcagcca tgcacggact			1651
107	cgtttccaga ggttaattatg agcgcctacc agccaggcca cccagccgtg ggaggaagg			1711
108	ggcgtggcaa ggggtgggca cattgggtgc tttgcgaaag gaaaattgac ccggaagttc			1771
109	ctgtataaaa tgtcacaata aaacgaatga atgaaaaaaaaaaaaaaa a			1822
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111	<211> LENGTH: 431			
112	<212> TYPE: PRT			
113	<213> ORGANISM: Homo sapiens			
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116	1 5 10 15			
117	Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser			
118	20 25 30			
119	Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser			
120	35 40 45			
121	Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu			
122	50 55 60			
123	Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro			
124	65 70 75 80			
125	Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly			
126	85 90 95			
127	Gly Pro Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser			
128	100 105 110			
129	Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr			
130	115 120 125			
131	Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys			
132	130 135 140			
133	Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu			
134	145 150 155 160			
135	Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile			
136	165 170 175			
137	Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile			
138	180 185 190			
139	Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu			
140	195 200 205			
141	Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu			
142	210 215 220			
143	Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg			
144	225 230 235 240			

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145 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser  
 146 245 250 255  
 147 ·Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn  
 148 260 265 270  
 149 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe  
 150 275 280 285  
 151 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser  
 152 290 295 300  
 153 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu  
 154 305 310 315 320  
 155 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr  
 156 325 330 335  
 157 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu  
 158 340 345 350  
 159 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn  
 160 355 360 365  
 161 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His  
 162 370 375 380  
 163 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln  
 164 385 390 395 400  
 165 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile  
 166 405 410 415  
 167 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His  
 168 420 425 430  
 169 <210> SEQ ID NO 3  
 170 <211> LENGTH: 102  
 171 <212> TYPE: PRT  
 172 <213> ORGANISM: Artificial Sequence  
 173 <220> FEATURE:  
 174 <223> OTHER INFORMATION: Description of Artificial Sequence: OPX  
 175 <220> FEATURE:  
 176 <223> OTHER INFORMATION: each Xaa is independently selected from a group of  
 177 one or more specified amino acids as defined in  
 178 the specification  
 179 <400> SEQUENCE: 3  
 W--> 180 Cys Xaa Xaa His Glu Leu Tyr Val Ser Phe Xaa Asp Leu Gly Trp Xaa  
 181 1 5 10 15  
 W--> 182 Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly  
 183 20 25 30  
 W--> 184 Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala  
 185 35 40 45  
 W--> 186 Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys  
 187 50 55 60  
 W--> 188 Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa  
 189 65 70 75 80  
 W--> 190 Asp Xaa Ser Xaa Asn Val Ile Leu Xaa Lys Xaa Arg Asn Met Val Val  
 191 85 90 95  
 W--> 192 Xaa Ala Cys Gly Cys His  
 193 100  
 194 <210> SEQ ID NO 4

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RAW SEQUENCE LISTING  
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TIME: 09:48:39

Input Set: I540466.RAW

```

195 <211> LENGTH: 97
196 <212> TYPE: PRT
197 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Description of Artificial Sequence: Generic-Seq-7
200 <220> FEATURE:
201 <223> OTHER INFORMATION: each Xaa is independently selected from a group of
202 one or more specified amino acids as defined in
203 the specification
204 <400> SEQUENCE: 4
W--> 205 Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa Xaa Xaa Xaa Xaa Xaa
206 1 5 10 15
W--> 207 Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Pro
208 20 25 30
W--> 209 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala Xaa Xaa Xaa Xaa Xaa Xaa
210 35 40 45
W--> 211 Xaa Cys Cys Xaa Pro
212 50 55 60
W--> 213 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
214 65 70 75 80
W--> 215 Val Xaa Leu Xaa Xaa Xaa Xaa Met Xaa Val Xaa Xaa Cys Xaa Cys
216 85 90 95
W--> 217 Xaa
218 <210> SEQ ID NO 5
219 <211> LENGTH: 102
220 <212> TYPE: PRT
221 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: Description of Artificial Sequence: Generic-Seq-8
224 <220> FEATURE:
225 <223> OTHER INFORMATION: each Xaa is independently selected from a group of
226 one or more specified amino acids as defined in the
227 specification
228 <400> SEQUENCE: 5
W--> 229 Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa
230 1 5 10 15
W--> 231 Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly
232 20 25 30
W--> 233 Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala
234 35 40 45
W--> 235 Xaa Xaa
236 50 55 60
W--> 237 Xaa Cys Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa
238 65 70 75 80
W--> 239 Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val
240 85 90 95
W--> 241 Xaa Xaa Cys Xaa Cys Xaa
242 100
243 <210> SEQ ID NO 6

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Please Note: <211> LENGTH: 97

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I540466.RAW

## Line ? Error/Warning

## Original Text

180 W "N" or "Xaa" used: Feature required  
 182 W "N" or "Xaa" used: Feature required  
 184 W "N" or "Xaa" used: Feature required  
 186 W "N" or "Xaa" used: Feature required  
 188 W "N" or "Xaa" used: Feature required  
 190 W "N" or "Xaa" used: Feature required  
 192 W "N" or "Xaa" used: Feature required  
 205 W "N" or "Xaa" used: Feature required  
 207 W "N" or "Xaa" used: Feature required  
 209 W "N" or "Xaa" used: Feature required  
 211 W "N" or "Xaa" used: Feature required  
 213 W "N" or "Xaa" used: Feature required  
 215 W "N" or "Xaa" used: Feature required  
 217 W "N" or "Xaa" used: Feature required  
 229 W "N" or "Xaa" used: Feature required  
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 235 W "N" or "Xaa" used: Feature required  
 237 W "N" or "Xaa" used: Feature required  
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 241 W "N" or "Xaa" used: Feature required  
 254 W "N" or "Xaa" used: Feature required  
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Cys Xaa Xaa His Glu Leu Tyr Val Ser Phe X  
 Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa A  
 Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met A  
 Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa P  
 Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala X  
 Asp Xaa Ser Xaa Asn Val Ile Leu Xaa Lys X  
 Xaa Ala Cys Gly Cys His  
 Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp X  
 Pro Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa G  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His A  
 Xaa X  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa X  
 Val Xaa Leu Xaa Xaa Xaa Xaa Met Xaa V  
 Xaa  
 Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe X  
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 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X  
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